

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=9; day=3; hr=10; min=25; sec=45; ms=413;]

=====

Application No: 10518072 Version No: 2.0

Input Set:

Output Set:

Started: 2010-08-23 19:07:34.756
Finished: 2010-08-23 19:07:45.969
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 213 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 150
Actual SeqID Count: 150

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)

Input Set:

Output Set:

Started: 2010-08-23 19:07:34.756
Finished: 2010-08-23 19:07:45.969
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 213 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 150
Actual SeqID Count: 150

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (35)
W 402	Undefined organism found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)

Input Set:

Output Set:

Started: 2010-08-23 19:07:34.756
Finished: 2010-08-23 19:07:45.969
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 213 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 150
Actual SeqID Count: 150

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (44)
W 213	Artificial or Unknown found in <213> in SEQ ID (45)
W 213	Artificial or Unknown found in <213> in SEQ ID (46)
W 213	Artificial or Unknown found in <213> in SEQ ID (47)
W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 213	Artificial or Unknown found in <213> in SEQ ID (50)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 213	Artificial or Unknown found in <213> in SEQ ID (58)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 402	Undefined organism found in <213> in SEQ ID (60) This error has occurred more than 20 times, will not be displayed
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (63)
E 300	Invalid codon found Phe SEQID (63) POS: 432
E 300	Invalid codon found Leu SEQID (63) POS: 435
E 300	Invalid codon found Phe SEQID (63) POS: 438
E 300	Invalid codon found Leu SEQID (63) POS: 441
E 300	Invalid codon found Gly SEQID (63) POS: 444
E 300	Invalid codon found Thr SEQID (63) POS: 447

Input Set:

Output Set:

Started: 2010-08-23 19:07:34.756
Finished: 2010-08-23 19:07:45.969
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 213 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 150
Actual SeqID Count: 150

Error code	Error Description			
E 300	Invalid codon found	Pro SEQID	(63)	POS: 450
E 300	Invalid codon found	Glu SEQID	(63)	POS: 453
E 300	Invalid codon found	Ala SEQID	(63)	POS: 456
E 355	Empty lines found between the amino acid numbering and the			
E 321	No. of Bases conflict, this line has no nucleotides	SEQID	(64)	
E 300	Invalid codon found	Pro SEQID	(64)	POS: 289
E 300	Invalid codon found	Lys SEQID	(64)	POS: 292
E 300	Invalid codon found	Asn SEQID	(64)	POS: 295
E 300	Invalid codon found	Ala SEQID	(64)	POS: 298
E 300	Invalid codon found	Ala SEQID	(64)	POS: 301
E 300	Invalid codon found	Val SEQID	(64)	POS: 304
E 300	Invalid codon found	Met SEQID	(64)	POS: 307
E 300	Invalid codon found	Leu SEQID	(64)	POS: 310
E 300	Invalid codon found	Trp SEQID	(64)	POS: 313
E 300	Invalid codon found	Ile SEQID	(64)	POS: 316
E 300	Invalid codon found	Phe SEQID	(64)	POS: 319 This error has occurred more than 20 times, will not be displayed
E 336	Empty lines found between the proteins and the dna			
E 336	Empty lines found between the proteins and the dna			
E 336	Empty lines found between the proteins and the dna			
E 336	Empty lines found between the proteins and the dna			
E 355	Empty lines found between the amino acid numbering and the			

Input Set:

Output Set:

Started: 2010-08-23 19:07:34.756
Finished: 2010-08-23 19:07:45.969
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 213 ms
Total Warnings: 103
Total Errors: 121
No. of SeqIDs Defined: 150
Actual SeqID Count: 150

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (78)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (83)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (97)
W 213	Artificial or Unknown found in <213> in SEQ ID (123)
W 213	Artificial or Unknown found in <213> in SEQ ID (124)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (125)
W 213	Artificial or Unknown found in <213> in SEQ ID (128)
W 213	Artificial or Unknown found in <213> in SEQ ID (129) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Weill, Mylene
Fort, Philippe
Raymond, Michel
Pasteur, Nicole

<120> NOVEL ACETYLCHOLINESTERASE GENE RESPONSIBLE FOR
INSECTICIDE RESISTANCE AND APPLICATIONS THEREOF

<130> 263365US0XPCT

<140> 10518072
<141> 2010-08-23

<150> FR 02/07622
<151> 2002-06-20

<150> FR 02/13799
<151> 2002-11-05

<160> 150

<170> PatentIn version 2.1

<210> 1
<211> 524
<212> PRT
<213> Anopheles gambiae

<400> 1
Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg Ile Arg Gly Ile Thr
1 5 10 15

Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val Trp Leu Gly Ile Pro
20 25 30

Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe Arg His Pro Arg Pro
35 40 45

Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr Pro Pro Asn Ser
50 55 60

Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp Phe Pro Gly Ala Thr
65 70 75 80

Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp Cys Leu Tyr Ile Asn
85 90 95

Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala Ala Val Met Leu Trp
100 105 110

Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala Thr Leu Asp Val Tyr
115 120 125

Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val Ile Val Val Ser Leu
130 135 140

Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe Leu Gly Thr Pro Glu
145 150 155 160

Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn Leu Ala Leu Arg Trp
165 170 175

Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp Pro Ser Arg Val Thr
180 185 190

Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val Ser Leu His Leu Leu
195 200 205

Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala Ile Leu Gln Ser Gly
210 215 220

Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg Glu Glu Ala Thr Leu
225 230 235 240

Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys Pro His Glu Pro Ser
245 250 255

Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly Lys Asp Pro His Val
260 265 270

Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile Cys Glu Phe Pro Phe
275 280 285

Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu Thr Pro Gln Arg Ser
290 295 300

Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile Leu Thr Gly Ser Asn
305 310 315 320

Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr Leu Thr Glu Leu Leu
325 330 335

Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu Glu Phe Leu Gln Ala
340 345 350

Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala Ala Arg Gln Ala Ile
355 360 365

Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp Asn Pro Asn Ser Asn
370 375 380

Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr His Phe Thr Cys Asn
385 390 395 400

Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu Gly Asn Asn Val Tyr
405 410 415

Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn Pro Trp Pro Arg Trp
420 425 430

Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr Val Phe Gly Glu Pro
435 440 445

Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu Lys Asp Phe Ser Arg
450 455 460

Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys Thr Gly Asn Pro Asn
465 470 475 480

Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp Pro Lys His Thr Ala
485 490 495

His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn Thr Ser Phe Val Gly
500 505 510

Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp Lys
515 520

<210> 2

<211> 1932

<212> DNA

<213> Anopheles gambiae

<220>

<221> CDS

<222> (1)..(1932)

<400> 2

atg ttt gtg tgt tgt ttt ttc ttt ctc tct ctc tct ttc tgt ggt tcc 48
Met Phe Val Cys Cys Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser
1 5 10 15

aac att tca gac gca ttt ttt aca cca tat ata ggt cac ggt gag tcc 96
Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser
20 25 30

gta cga att ata gat gcc gag ttg ggc acg ctc gag cat gtc cac agt 144
Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser
35 40 45

gga gca acg ccg cgg cga cgc ggc ctg acg agg cgc gag tca aac tcg 192
Gly Ala Thr Pro Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser
50 55 60

gac gcg aac gac aac gat ccg ctg gtg gtc aac acg gat aag ggg cgc 240
Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg
65 70 75 80

atc cgc ggc att acg gtc gat gcg ccc agc ggc aag aag gtg gac gtg 288
Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val
85 90 95

tgg ctc ggc att ccc tac gcc cag ccg ccg gtc ggg ccg cta cgg ttc 336
Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe

100	105	110	
cgt cat ccg ccg gcc gaa aag tgg acc ggc gtg ctg aac acg acc Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr			384
115	120	125	
aca ccg ccc aac agc tgc gtg cag atc gtg gac acc gtg ttc ggc gac Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp			432
130	135	140	
ttc ccg ggc gcg acc atg tgg aac ccg aac acg ccc ctg tcc gag gac Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp			480
145	150	155	160
tgt ctg tac att aac gtg gtg gca ccg cga ccc cgg ccc aag aat gcg Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala			528
165	170	175	
gcc gtc atg ctg tgg atc ttc ggc ggc ttc tac tcc ggc acc gcc Ala Val Met Leu Trp Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala			576
180	185	190	
acc ctg gac gtg tac gac cac ccg gcg ctt gcg tcg gag gag aac gtg Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val			624
195	200	205	
atc gtg gtg tcg ctg cag tac cgc gtg gcc agt ctg ggc ttc ctg ttt Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe			672
210	215	220	
ctc ggc acc ccg gaa gcg ccg ggc aat gcg gga ctg ttc gat cag aac Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn			720
225	230	235	240
ctt gcg cta cgc tgg gtg cgg gac aac att cac ccg ttc ggt ggc gat Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp			768
245	250	255	
ccg tcg cgt gtg aca ctg ttc ggc gag agt gcc ggt gcc gtc tcg gtg Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val			816
260	265	270	
tcg ctg cat ctg ctg tcc gcc ctt tcc cgc gat ctg ttc cag ccg gcc Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala			864
275	280	285	
atc ctg cag agc ggc tcg ccg acg gca ccg tgg gca ttg gta tcg cgc Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg			912
290	295	300	
gag gaa gcc aca cta aga gca ctg ccg ttg gcc gag gcg gtc ggc tgc Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys			960
305	310	315	320
ccg cac gaa ccg agc aag ctg agc gat gcg gtc gag tgc ctg cgc ggc Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly			1008

325	330	335	
aag gac ccg cac gtg ctg gtc aac aac gag tgg ggc acg ctc ggc att Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile 340	345	350	1056
tgc gag ttc ccg ttc gtg ccg gtg gtc gac ggt gcg ttc ctg gac gag Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu 355	360	365	1104
acg ccg cag cgt tcg ctc gcc agc ggg cgc ttc aag aag acg gag atc Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile 370	375	380	1152
ctc acc ggc agc aac acg gag gag ggc tac tac atc atc tac tac Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr 385	390	395	1200
400			
ctg acc gag ctg ctg cgc aag gag gag ggc gtg acc gtg acg cgc gag Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu 405	410	415	1248
gag ttc ctg cag gcg gtg cgc gag ctc aac ccg tac gtg aac ggg gcg Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala 420	425	430	1296
435			
gcc cgg cag gcg atc gtg ttc gag tac acc gac tgg acc gag ccg gac Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp 440	445		1344
450			
aac ccg aac agc aac ccg gac gcg ctg gac aag atg gtg ggc gac tat Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr 455	460		1392
465			
cac ttc acc tgc aac gtg aac gag ttc gcg cag cgg tac gcc gag gag His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu 470	475	480	1440
485			
ggc aac aac gtc tac atg tat ctg tac acg cac cgc agc aaa ggc aac Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn 490	495		1488
500			
ccg tgg ccg cgc tgg acg ggc gtg atg cac ggc gac gag atc aac tac Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr 505	510		1536
515			
gtg ttc ggc gaa ccg ctc aac ccc acc ctc ggc tac acc gag gac gag Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp Glu 520	525		1584
530			
aaa gac ttt agc ccg aag atc atg cga tac tgg tcc aac ttt gcc aaa Lys Asp Phe Ser Arg Lys Ile Met Arg Tyr Trp Ser Asn Phe Ala Lys 535	540		1632
545			
acc ggg aat cca aat ccc aac acg gcc agc agc gaa ttc ccc gag tgg Thr Gly Asn Pro Asn Pro Asn Thr Ala Ser Ser Glu Phe Pro Glu Trp 550	555	560	1680

ccc aag cac acc gcc cac gga cgg cac tat ctg gag ctg ggc ctc aac			1728
Pro Lys His Thr Ala His Gly Arg His Tyr Leu Glu Leu Gly Leu Asn			
565	570	575	
acg tcc ttc gtc ggt cgg ggc cca cgg ttg agg cag tgt gcc ttc tgg			1776
Thr Ser Phe Val Gly Arg Gly Pro Arg Leu Arg Gln Cys Ala Phe Trp			
580	585	590	
aag aag tac ctt ccc cag cta gtt gca gct acc tcg aac cta cca ggg			1824
Lys Lys Tyr Leu Pro Gln Leu Val Ala Ala Thr Ser Asn Leu Pro Gly			
595	600	605	
cca gca ccg cct agt gaa ccg tgc gaa agc agc gca ttt ttt tac cga			1872
Pro Ala Pro Pro Ser Glu Pro Cys Glu Ser Ser Ala Phe Phe Tyr Arg			
610	615	620	
cct gat ctg atc gtg ctg ctg gtg tcg ctg ctt acg gcg acc gtc aga			1920
Pro Asp Leu Ile Val Leu Leu Val Ser Leu Leu Thr Ala Thr Val Arg			
625	630	635	640
ttc ata caa taa			1932
Phe Ile Gln			
<210> 3			
<211> 643			
<212> PRT			
<213> Anopheles gambiae			
<400> 3			
Met Phe Val Cys Cys Phe Phe Phe Leu Ser Leu Ser Phe Cys Gly Ser			
1	5	10	15
Asn Ile Ser Asp Ala Phe Phe Thr Pro Tyr Ile Gly His Gly Glu Ser			
20	25	30	
Val Arg Ile Ile Asp Ala Glu Leu Gly Thr Leu Glu His Val His Ser			
35	40	45	
Gly Ala Thr Pro Arg Arg Gly Leu Thr Arg Arg Glu Ser Asn Ser			
50	55	60	
Asp Ala Asn Asp Asn Asp Pro Leu Val Val Asn Thr Asp Lys Gly Arg			
65	70	75	80
Ile Arg Gly Ile Thr Val Asp Ala Pro Ser Gly Lys Lys Val Asp Val			
85	90	95	
Trp Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly Pro Leu Arg Phe			
100	105	110	
Arg His Pro Arg Pro Ala Glu Lys Trp Thr Gly Val Leu Asn Thr Thr			
115	120	125	
Thr Pro Pro Asn Ser Cys Val Gln Ile Val Asp Thr Val Phe Gly Asp			

130	135	140
Phe Pro Gly Ala Thr Met Trp Asn Pro Asn Thr Pro Leu Ser Glu Asp		
145	150	155
Cys Leu Tyr Ile Asn Val Val Ala Pro Arg Pro Arg Pro Lys Asn Ala		
165	170	175
Ala Val Met Leu Trp Ile Phe Gly Gly Phe Tyr Ser Gly Thr Ala		
180	185	190
Thr Leu Asp Val Tyr Asp His Arg Ala Leu Ala Ser Glu Glu Asn Val		
195	200	205
Ile Val Val Ser Leu Gln Tyr Arg Val Ala Ser Leu Gly Phe Leu Phe		
210	215	220
Leu Gly Thr Pro Glu Ala Pro Gly Asn Ala Gly Leu Phe Asp Gln Asn		
225	230	235
240		
Leu Ala Leu Arg Trp Val Arg Asp Asn Ile His Arg Phe Gly Gly Asp		
245	250	255
Pro Ser Arg Val Thr Leu Phe Gly Glu Ser Ala Gly Ala Val Ser Val		
260	265	270
Ser Leu His Leu Leu Ser Ala Leu Ser Arg Asp Leu Phe Gln Arg Ala		
275	280	285
Ile Leu Gln Ser Gly Ser Pro Thr Ala Pro Trp Ala Leu Val Ser Arg		
290	295	300
Glu Glu Ala Thr Leu Arg Ala Leu Arg Leu Ala Glu Ala Val Gly Cys		
305	310	315
320		
Pro His Glu Pro Ser Lys Leu Ser Asp Ala Val Glu Cys Leu Arg Gly		
325	330	335
Lys Asp Pro His Val Leu Val Asn Asn Glu Trp Gly Thr Leu Gly Ile		
340	345	350
Cys Glu Phe Pro Phe Val Pro Val Val Asp Gly Ala Phe Leu Asp Glu		
355	360	365
Thr Pro Gln Arg Ser Leu Ala Ser Gly Arg Phe Lys Lys Thr Glu Ile		
370	375	380
Leu Thr Gly Ser Asn Thr Glu Glu Gly Tyr Tyr Phe Ile Ile Tyr Tyr		
385	390	395
400		
Leu Thr Glu Leu Leu Arg Lys Glu Glu Gly Val Thr Val Thr Arg Glu		
405	410	415
Glu Phe Leu Gln Ala Val Arg Glu Leu Asn Pro Tyr Val Asn Gly Ala		
420	425	430

Ala Arg Gln Ala Ile Val Phe Glu Tyr Thr Asp Trp Thr Glu Pro Asp
435 440 445

Asn Pro Asn Ser Asn Arg Asp Ala Leu Asp Lys Met Val Gly Asp Tyr
450 455 460

His Phe Thr Cys Asn Val Asn Glu Phe Ala Gln Arg Tyr Ala Glu Glu
465 470 475 480

Gly Asn Asn Val Tyr Met Tyr Leu Tyr Thr His Arg Ser Lys Gly Asn
485 490 495

Pro Trp Pro Arg Trp Thr Gly Val Met His Gly Asp Glu Ile Asn Tyr
500 505 510

Val Phe Gly Glu Pro Leu Asn Pro Thr Leu Gly Tyr Thr Glu Asp G